

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Holtzman, Douglas A.  
 Application No.: 09/782,980  
 Filed: February 13, 2001  
 For: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND STMST PROTEIN  
 AND NUCLEIC ACID MOLECULES AND USES THEREFOR

Group No.: 1652

Examiner: Maryam Monshipouri, Ph.D.

Commissioner for Patents  
 Washington, DC 20231

RESPONSE TO RESTRICTION REQUIREMENT

Dear Madam:

REMARKS

In response to the Restriction Requirement dated June 12, 2003 (Paper No. 11), Applicants hereby elect Group 9b, drawn to isolated DNA sequences encoding human STMST-2 polypeptides, host cells, kits comprising said sequences, and methods of expressing said sequences (claims 1-7, 12, 18, and 53-54), with traverse. This election is made without prejudice to Applicant's right to pursue the non-elected subject matter in other applications in the event a generic claim is not found allowable.

Applicants respectfully traverse the present restriction and reserve the right to petition therefrom under 37 C.F.R. § 1.144 and for the reasons set forth below.

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10\*

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37 C.F.R. SECTION 1.8(a)

37 C.F.R. SECTION 1.10\*

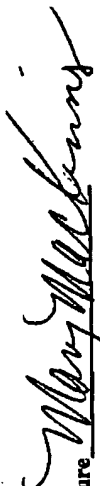
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Date: July 14, 2003

Mary MacKinnon

(type or print name of person certifying)

#12  
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**Elected as Separate Species of a Common Genus**

Applicants submit that the separate nucleic acid sequences encoding SEQ ID NOs:71 and 74 (STMST-1 and STMST-2, respectively) should be examined together, as species of a common genus. As seen in the enclosed protein sequence alignment (Exhibit A), the sequences of SEQ ID NOs:71 and 74 (and the nucleic acid sequences encoding them) are related in that SEQ ID NO:74 (STMST-2), which is a 609 residue protein, comprises the majority portion of SEQ ID NO:71 (STMST-1), which is a 297 residue protein. Both protein sequences share the first 262 residues, which constitute over 88% of the entire length of the STMST-1 protein. The nucleic acid sequence encoding the protein sequences are even more similar, as evidenced by the enclosed alignment of the open reading frame encoding STMST-1 and a truncated version of the open reading frame encoding STMST-2 (Exhibit B, showing 93% sequence identity over the length of the STMST-1 open reading frame).

The inclusion of both nucleic acids which encode SEQ ID NOs:71 and 74 in the current election does not pose a serious examination burden on the Examiner. In fact, it would require virtually the same search and examination, since searching and examining nucleic acids that encode SEQ ID NO:74 includes by necessity a search and examination of the nucleic acids that encode SEQ ID NO:71 (SEQ ID NO:71 shares residues 1-262 of SEQ ID NO:74).

This paper is being filed timely, as it is believed that no extensions of time are required. In the event any extensions of time are deemed necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Entry of the remarks made herein is respectfully requested.

July 14, 2003

Respectfully submitted,

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>STMST1
>STMST2
scoring matrix: BLOSUM50, gap penalties: -12/-2
46.8% identity; Global alignment score: 1198

STMST2 MSDERRLPGS AVGMLVCGGLSILLANAWGILSVGAKQKKWKPLEFLCLTLAATHMLNVAVP
10 20 30 40 50 60
STMST2 MSDERRLPGS AVGMLVCGGLSILLANAWGILSVGAKQKKWKPLEFLCLTLAATHMLNVAVP
10 20 30 40 50 60
STMST1 IATYSVVQLRRQRPDFEWN EGLCKVFVSTFYTLTATCFSVTSLSYHRMMVWCWPFVNYRL
70 80 90 100 110 120
STMST2 IATYSVVQLRRQRPDFEWN EGLCKVFVSTFYTLTATCFSVTSLSYHRMMVWCWPFVNYRL
70 80 90 100 110 120
STMST1 SNAKKQAVHTVMGIWVSFILSALPAVGWHDTSERFTHGCRFIVAEIGLGFGVCFLLLV
130 140 150 160 170 180
STMST2 SNAKKQAVHTVMGIWVSFILSALPAVGWHDTSERFTHGCRFIVAEIGLGFGVCFLLLV
130 140 150 160 170 180
STMST1 GGSVAMGVICTAIALFQTLAVQVGRQADHRAFTVPTIVVEDAQGKRSSIDGSEPAKTSI
190 200 210 220 230 240
STMST2 GGSVAMGVICTAIALFQTLAVQVGRQADHRAFTVPTIVVEDAQGKRSSIDGSEPAKTSI
190 200 210 220 230 240
STMST1 QTTGLVTVTFIYDCLMGFPVL-----D-STP-----IP-----
250 260
STMST2 QTTGLVTVTFIYDCLMGFPVLVVSFSSLRADASAFWMALCVLWCSVAQALLPFLWAC
250 260 270 280 290 300
STMST1 -----ERS-----
270
STMST2 DRYRADLKAVREKCMALMANDESDDETSLEGGISPLVLERSLDYGYGGDFVALDRMAK
310 320 330 340 350 360
STMST1 ---AVRQ-----ED-----WG-----
280
STMST2 YEISALEGGLPOLYPLRPLQEDKMOVLQVPPTRRFSHDDADVWAAVPLPAFLPRWGSGED
370 380 390 400 410 420
STMST1 -----KDQPE-----
STMST2 LAALAHVLPA GPERRRRASLLAFADAPPSRARRRSAESLLSLRTSALDSGPRGARDSPP
430 440 450 460 470 480
STMST1 G-----FH-----
STMST2 GSPRRRPGGPRRSASASLLPDFAFALTAFECEPQALRRPPGPFPAAPADGADPGGEAFTP
490 500 510 520 530 540
290
STMST1 PSSRO-----

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STMST1 --DCL---P  
: :  
STMST2 HSDSLGSAS

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>stmst1
>stmst2 (truncated)
scoring matrix: DNA, gap penalties: -16/-4
93.0% identity; Global alignment score: 3863

      10   20   30   40   50   60
/tmp/s  ATGAGTGATGAGCGCGGCTGCCCTGGCAGTGCAGTGGCTGGCTGGTATGTGGGGGCCCTC
      :
      :
      :
stmst2  ATGAGTGATGAGCGCGGCTGCCCTGGCAGTGCAGTGGCTGGCTGGTATGTGGGGGCCCTC
      10   20   30   40   50   60

      70   80   90   100  110  120
/tmp/s  TCCCTGCTGGCCCAATGCCCTGGGGCATCCTCAGCGTTGGCGCCCAAGCAGAGAAGTGGAG
      :
      :
      :
stmst2  TCCCTGCTGGCCCAATGCCCTGGGGCATCCTCAGCGTTGGCGCCCAAGCAGAGAAGTGGAG
      70   80   90   100  110  120

      130  140  150  160  170  180
/tmp/s  CCCTTGGAGTTCCTGCTGTGTACGCTCGCGGCCACCCACATGCTAAATGTGGCCGCTGCC
      :
      :
      :
stmst2  CCCTTGGAGTTCCTGCTGTGTACGCTCGCGGCCACCCACATGCTAAATGTGGCCGCTGCC
      130  140  150  160  170  180

      190  200  210  220  230  240
/tmp/s  ATCGCCACCTACTCCGTGGTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
      :
      :
      :
stmst2  ATCGCCACCTACTCCGTGGTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
      190  200  210  220  230  240

      250  260  270  280  290  300
/tmp/s  GGTCCTGCAAGGTCTTCGTGTCCACCTTCTACACCCCTCACCCTGGCCACCTGTTTCTCT
      :
      :
      :
stmst2  GGTCCTGCAAGGTCTTCGTGTCCACCTTCTACACCCCTCACCCTGGCCACCTGTTTCTCT
      250  260  270  280  290  300

      310  320  330  340  350  360
/tmp/s  GTCACCTCCCTCTCTTACCACCGCATGTGGATGGTCTGCTGGCTGTCAACTACCGGCTG
      :
      :
      :
stmst2  GTCACCTCCCTCTCTTACCACCGCATGTGGATGGTCTGCTGGCTGTCAACTACCGGCTG
      310  320  330  340  350  360

      370  380  390  400  410  420
/tmp/s  AGCAATGCCAAGAAGCAGCGGCTGCACACAGTCAAGGGTATCTGGATGGTGTCTTCATC
      :
      :
      :
stmst2  AGCAATGCCAAGAAGCAGCGGCTGCACACAGTCAAGGGTATCTGGATGGTGTCTTCATC
      370  380  390  400  410  420

      430  440  450  460  470  480
/tmp/s  CTGTGCGGCCCTTCCCTGCCGTTGGCTGGCAGCAGCAGCGGCGCTTCTACACCCATGGC
      :
      :
      :
stmst2  CTGTGCGGCCCTTCCCTGCCGTTGGCTGGCAGCAGCAGCGGCGCTTCTACACCCATGGC
      430  440  450  460  470  480

      490  500  510  520  530  540
/tmp/s  TGCCGCTTCATCGTGGCTGAGATCGGCCCTGGGCTTGGCGTCTGCTTCTGCTGCTGGTG
      :
      :
      :
stmst2  TGCCGCTTCATCGTGGCTGAGATCGGCCCTGGGCTTGGCGTCTGCTTCTGCTGCTGGTG
      490  500  510  520  530  540

      550  560  570  580  590  600
/tmp/s  GCGGCGAGCGTGGCCCATGGCGGTGATCTGCACAGCCATCGCCCTCTTCCAGACGCGTGGCC
```

/tmp/s	610	620	630	640	650	660
stms2	610	620	630	640	650	660
/tmp/s	670	680	690	700	710	720
stms2	670	680	690	700	710	720
/tmp/s	730	740	750	760	770	780
stms2	730	740	750	760	770	780
/tmp/s	790	800	810	820	830	
stms2	790	800	810	820	830	
/tmp/s	840	850	860	870	880	890
stms2	840	850	860	870	880	890

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**PATENT**

Practitioner's Docket No. MP100-544OMNIM

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#### Submitted herewith:

Response to Restriction Requirement	(2 pages)
Exhibit A	(2 pages)
Exhibit B	(2 pages)
<b>Total</b>	<b>(7 pages-including fax cover sheet)</b>

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